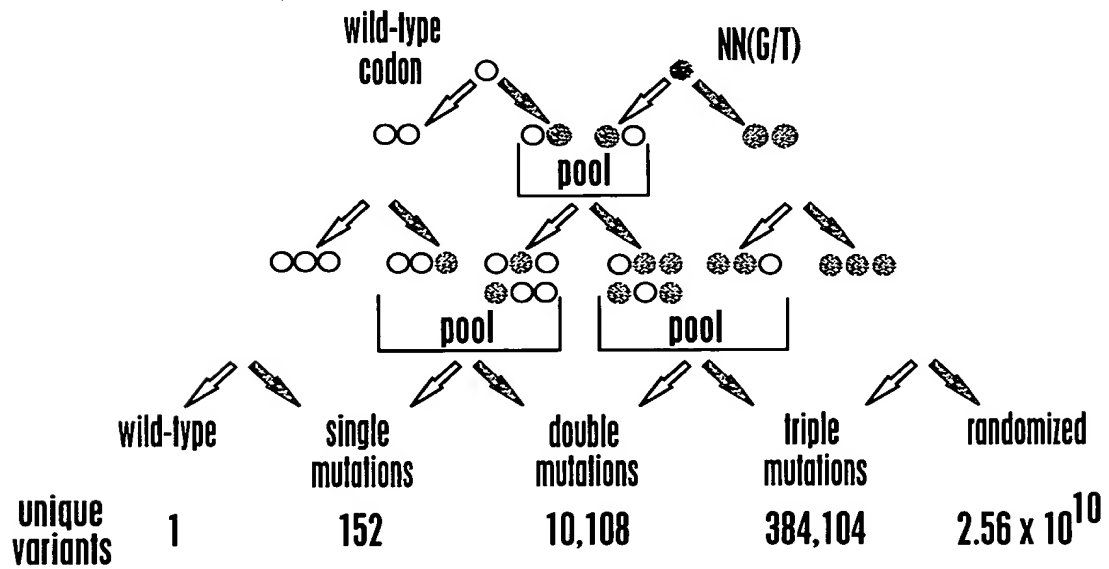


Figure 6

Figure 7



T7 primer

TTAATACGACTCACTATAGGG AGACGGG AAG CTT AAG GTG CAC GGC CCA CGT GGA TCG ATC GCG CGC AGA TCT TCG GAA

Hind 3

Bgl II

-28

Met Asp Ser Lys Val Thr Ile Ile Cys Ile Arg Phe Leu Phe Trp Phe Leu Leu Cys Met Leu Ile Gly Lys Ser His Thr
GCC ACC ATG GAT AGC AAA GTC ACA ATC ATA TGC ATC AGA TTT CTC TTT TGG TTT CTT TTG CTC TGC ATG CTT ATT GGG AAG TCA CAT ACT

+1 NcoI

10

CHO

20

Sph I

30

Glu Asp Asp Ile Ile Ala Thr Lys Lys Asn Gly Lys Val Arg Gly Met Asn Leu Thr Val Phe Gly Thr Val Thr Ala Phe Leu Gly
GAA GAT GAC ATC ATA ATT GCA ACA AAG AAT GCA AAA GTC AGA GGG ATG AAC TTG ACA GTT TTT GGT GGC AGG GTA ACA GCC TTT CTT GGA 90

40

50

CHO

60

Ile Pro Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys
ATT CCC TAT GCA CAG CCA CCT CTT GGT AGA CTT CGA TTC AAA AAG CCA CAG TCT CTG ACC AAG TGG TCT GAT ATT TGG AAT GCC ACA AAA 180

Acc I Taq I

80

90

Tyr Ala Asn Ser Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu Met Trp Asn Pro Asn Thr Asp Leu Ser Glu
TAT GCA AAT TCT TGC TGT CAG AAC ATA GAT CAA AGT TTT CCA GGC TTC CAT GGA TCA GAG ATG TGG AAC CCA AAC ACT GAC CTC AGT GAA 270

100

110

117

120

Asp Cys Leu Tyr Leu Asn Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp Ile Tyr Gly Gly Phe Gln Thr
GAC TGT TTA TAT CTA AAT GTA TGG ATT CCA GCA CCT AAA CCA AAA AAT GCC ACT GTA TTG ATA TGG ATT TAT GGT GGT TTT CAA ACT 360

130

140

150

Gly Thr Ser Ser Leu His Val Tyr Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met Asn Tyr Arg Val Gly Ala
GGA ACA TCA TCT TTA CAT GTT TAT GAT GGC AAG TTT CTG GGT CGG GTT GAA AGA GTT ATT GTA GTG TCA ATG AAC TAT AGG GTG GGT GCC 450

Ava I

Figure 1A

25

160 Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln Trp Val Gln Lys 180
 CTA GGA TTC TTA GCT TTG CCA GGA AAT CCT GAG GCT CCA GGG AAC ATG GGT TTA TTT GAT CAA CAG TTG GCT CTT CAG TGG GTT CAA AAA 540
 170
 190 Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val Thr Leu phe Gly Glu SER Ala Gly Ala Ala Ser Val Ser Leu His Leu Leu Ser 210
 *
 200 AAT ATA GCA GCC TTT GGT GGA AAT CCT AAA AGT GTA ACT CTC TTT GGA GAA AGT GCA GCA GGT TCA GTT AGC CTG CAT TTG CTT TCT 630
 220
 230 Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser Gly Ser Phe Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 240
 CCT GGA ACC CAT TCA TTG TTC ACC AGA GCC ATT CTG CAA AGT GGT TCC TTT AAT GCT CCT TTG GCG GTA ACA TCT CTT TAT GAA GCT AGG 720
 CHO 250 CHO 260
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp pro Gln 270
 AAC AGA ACC TTG AAC TTA GCT AAA TTG ACT GGT TGC TCT AGA GAG AAT GAG ACT GAA ATA ATC AAG TGT CTT ACA AAT AAA GAT CCC CAA 810
 280 Xba I 290
 Glu Ile Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr 300
 GAA ATT CTT CTG AAT GAA GCA TTT GTT GTC CCC TAT GGG ACT CCT TTG TCA GTA AAC TTT GGT CCG ACC GTG GAT GGT GAT TTT CTC ACT 900
 310 320 Ava II 330
 Asp Met Pro Asp Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly Val Asn Lys Asp Glu Gly Thr Trp Phe Leu
 GAC ATG CCA GAC ATA TTA CTT GAA CTT GGA CAA TTT AAA AAA ACC CAG ATT TTG GTG GGT GTT AAT AAA GAT GAA GGG ACA TGG TTT TTA 990
 CHO

Figure 1B

340	Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu Gly Leu Lys Ile Phe Phe Pro Gly	350	360
	GTC TAT GGT GCT CCT GGC TTC AGC AAA GAT AAC AAT AGT ATC ATA ACT AGA AAA GAA TTT CAG GAA GGT TTA AAA ATA TTT TTT CCA GGA 1080		
370		Dra I SspI	390
	Val Ser Glu Phe Gly Lys Glu Ser Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn Tyr Arg Glu Ala Leu Gly	380	
	GTC ACT GAG TTT GGA AAG GAA TCC ATC CTT TTT CAT TAC ACA GAC TCG GTA GAT GAT CAG AGA CCT GAA AAC TAC CGT GAG GCC TTG GGT 1170		
400		Stu I	420
	Asp Val Val Gly Asp Tyr Asn Phe Ile Cys Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe Phe Tyr Tyr	410	
	GAT GTT GTT GGG GAT TAT AAT TTC ATA TGC CCT GGC CTT GAG TTC ACC AAG AAG TTC TCA GAA TGG GGA AAT AAT GCC TTT TTC TAC TAT 1260		
430			450
	Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro Leu	440	
	TTT GAA CAC CGA TCC TCC AAA CTT CCG TGG CCA GAA TGG ATG GGA GTG ATG CAT GGC TAT GAA ATT GAA TTT GTC TTT GGT TTA CCT CTG 1350		
460			480
	Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	470	
	GAA AGA AGA GAT AAT TAC ACA AAA GCC GAG GAA AAT TTG AGT AGA TCC ATA GTG AAA CGG TGG GCA AAT TTT GCA AAA TAT GGG AAT CCA 1440		
490			510
	Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile	500	
	AAT GAG ACT CAG AAC AAT AGC ACA AGC TGG CCT GTC TTC AAA AGC ACT GAA CAA AAA TAT CTA ACC TTG AAT ACA GAG TCA ACA AGA ATA 1530		
			Hinc II

Figure 1C

Met Thr Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu	520	530	540
ATG ACG AAA CTA CGT GGT CAA CAA TGT CGA TTC TGG ACA TCA TTT TTT CCA AAA GTC TTG GAA ATG ACA GGA AAT ATT GAT GAA GCA GAA			1620
	Taq I	Ssp I	
Trp Glu Trp Lys Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser		560	570
TGG GAG TGG AAA GCA GCA TTC CAT CGC TGG AAC AAT TAC ATG ATG GAC TGG AAA AAT CAA TTT AAC GAT TAC ACT AGC AAG AAA GAA AGT			1710
574			
Cys Val Gly Leu ***			
TGT GTG GGT CTC TAA TTA ATA GAT CTG TCA TGA TGA TCA TTG CAA TTG GAT CCA TAT ATA GGG CCC TATT CTATAGTGTACCTAAAT			
Ase I Bgl II	Bcl I	Bam HI, Eco01091, Apa I	Sp6 primer

Figure 1D

10 20 30 40 50
 EDDII IATKNGKVRGMNLT VFGGT VTAFLGI PYAQPP LGRLRFKKPQSLTK
 60 70 80 90 100
 WSDIWNATKYANSCCQNI DQSFPGFHGSEMWNPN TDLS EDCLYLNVWIPAP
 110 120 130 140 150
 KPKNATV LIWIYGGGFQTGT SSLHVYDGKFLARVERVIVVSMNYRVGALGF
 160 170 180 190 200
 LALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVT LFGESAGAASV
 210 220 230 240 250
 SLHLLSPGSHSLFTRAILQ SGSFNAPWAVTSLYEARNRTLNLAKLTGCSRE
 260 270 280 290 300
 NETEIIKCLR NKDPQEILLNEA FVVPYGTPLSVNFGPTVDGDFLT DMPDIL
 310 320 330 340 350
 LELGQFKKTQILVGVNKDEG TAFLVYGAPGFSKDNN SIITRKEFQEGLKIF
 360 370 380 390 400
 FPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKK
 410 420 430 440 450
 FSEWGNNAFFYYFEHRSSKLP WPEWMGMHGYEIEFVFGGLPLERRDNYTKA
 460 470 480 490 500 510
 EEILSR SIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLT LNTESTRI
 520 530 540 550 560
 MTKLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQF
 570
 NDYTSKKESCVGL

Figure 2

094839-060101
 T01090-6228460

1 tactgaatgt cagtgcagtc caatttacag gctggagcag cagctgcac ctcgatttcc
 61 ccgaagtatt acatgatttt cactccttgc aaactttacc atctttgttg cagagaatcg
 121 gaaatcaata tgcatagcaa agtcacaatc atatgcatca gatttctctt ttggtttctt
 181 ttgctctgca tgcttattgg gaagtcacat actgaagatg acatcataat tgcaacaaag
 241 aatggaaaag tcagagggat gaacttgaca gtttttggtg gcacggtaac agcctttctt
 301 ggaattccct atgcacagcc acctcttggg agacttcgat tcaaaaagcc acagtctctg
 361 accaagtggg ctgatatttg gaatgccaca aaatatgcaa attcttgctg tcagaacata
 421 gatcaaagtt ttccaggctt ccatggatca gagatgtgga acccaaacac tgacctcagt
 481 gaagactggt tatatctaaa tgtatggatt ccagcaccta aaccaaaaaa tgccactgta
 541 ttgatattga tttatgggtg tggttttcaa actggaacat catctttaca tgtttatgat
 601 ggcaagtttc tggtctgggt tgaaagagtt attgtagtgt caatgaacta tagggtgggt
 661 gccctaggat tcttagcttt gccaggaaat cctgaggctc cagggaacat ggggtttattt
 721 gatcaacagt tggtctttca gtgggttcaa aaaaatatag cagcctttgg tggaaatcct
 781 aaaagtgtaa ctctcttttg agaaagtgca ggagcagctt cagtttagctt gcatttgctt
 841 tctcctggaa gccattcatt gttcaccaga gccattctgc aaagtggatc cttaaatgct
 901 ccttgggcgg taacatctct ttatgaagct aggaacagaa cgttgaaactt agctaaattg
 961 actggttgct ctagagagaa tgagactgaa ataataagct gtcttagaaa taaagatccc
 1021 caagaaattc ttctgaatga agcatttggt gtcccctatg ggactccttt gtcagtaaac
 1081 tttggtccga ccgtggatgg tgattttctc actgacatgc cagacatatt acttgaactt
 1141 ggacaattta aaaaaacca gattttggtg ggtgttaata aagatgaagg gacagctttt
 1201 ttagtctatg gtgctcctgg cttcagcaaa gataacaata gtatcataac tagaaaagaa
 1261 tttcaggaag gtttaaaaat attttttcca ggagtgaagt agtttggaag ggaatccatc
 1321 ctttttcatt acacagactg ggtagatgat cagagacctg aaaactaccg tgaggccttg
 1381 ggtgatgttg ttggggatta taatttcata tgccctgcct tggagttcac caagaagttc
 1441 tcagaatggg gaaataatgc ctttttctac tattttgaac accgatcctc caaacttccg
 1501 tggccagaat ggatgggagt gatgcatggc tatgaaattg aatttgtctt tggtttacct
 1561 ctggaaagaa gagataatta cacaaaagcc gaggaattt tgagtagatc catagtgaag
 1621 cgggtgggcaa attttgcaaa atatgggaat ccaaatgaga ctcagaacaa tagcacaagc
 1681 tggcctgtct tcaaaagcac tgaacaaaaa tatctaacct tgaatacaga gtcaacaaga
 1741 ataatacgca aactacgtgc tcaacaatgt cgattctgga catcattttt tccaaaagtc
 1801 ttggaatga caggaaatat tgatgaagca gaatgggagt ggaaagcagg attccatcgc
 1861 tggacaatt acatgatgga ctggaaaaat caatttaacg attacactag caagaaagaa
 1921 agttgtgtgg gtctctaatt aatagattta ccctttatag aacatatttt ccttttagatc
 1981 aaggcaaaaa tatcaggagc ttttttacac acctactaaa aaagttatta tgtagctgaa

Figure 3A

2041 acaaaaatgc cagaaggata atattgattc ctcacatott taacttagta ttttacctag
2101 catttcaaaa cccaaattggc tagaacatgt ttaattaaat ttcacaatat aaagttctac
2161 agttaattat gtgcatatta aaacaatggc ctggttcaat ttctttcttt ccttaataaa
2221 ttttaagtttt ttccccccaa aattatcagt gctctgcttt tagtcacgtg tattttcatt
2281 accactcgta aaaaggatc ttttttaaata gaattaaata ttgaaacact gtacaccata
2341 gtttacaata ttatgtttcc taattaaaat aagaattgaa tgtcaatatg agatattaa
2401 ataagcacag aaaatc

Figure 3B

09748739.060404
TDTTDSO"6E2B4260

	1	10	20	30
HUMAN WILD-TYPE BChE	EDDIIIATKN	GKVRGMNLTV	FGGTVTAFLG	
HUMAN A VARIANT BChE	-----	-----	-----	
HUMAN J VARIANT BChE	-----	-----	-----	
HUMAN K VARIANT BChE	-----	-----	-----	
RAT BChE	EEDVIITTKT	GRVRGLSMPI	LG GTVTAFLG	
CAT BChE	EEDIIITTKN	GKVRGMNLTV	LDGTVTAFLG	
HORSE BChE	EEDIIITTKN	GKVRGMNLTV	LG GTVTAFLG	

	40	50	60	70	80	90	100
HUMAN WT	IPYAQPPLGR	LRFKKPQSLT	KWSDIWNATK	YANSCCQNID	QSFPGFHGSE	MWNPNTDLSE	DCLYLNWVWP
HUMAN A	-----	-----	-----	-----G	-----	-----	-----
HUMAN J	-----	-----	-----	-----	-----	-----	-----
HUMAN K	-----	-----	-----	-----	-----	-----	-----
RAT	IPYAQPPLGS	LRFKKPQPLN	KWPDVYNATK	YANSCYQNID	QAFPGFQGSE	MWNPNTNLSE	DCLYLNWVWP
CAT	IPYAQPPLGR	LRFKKPQFLT	KWSDIWNATK	YANSCYQNAD	QSFPGFPGSE	MWNPNTDLSE	DCLYLNWVWP
HORSE	IPYAQPPLGR	LRFKKPQSLT	KWSNIWNATK	YANSCYQNTD	QSFPGFLGSE	MWNPNTLSE	DCLYLNWVWP

	110	120	130	140	150	160	170
HUMAN WT	APKPKNATVL	IWIYGGGFQT	GTSSLHVDYG	KFLARVERVI	VVSMNYRVGA	LGFLALPGNP	EAPGNMGLFD
HUMAN A	-----	-----	-----	-----	-----	-----	-----
HUMAN J	-----	-----	-----	-----	-----	-----	-----
HUMAN K	-----	-----	-----	-----	-----	-----	-----
RAT	VPKPKNATVM	VWVYGGGFQT	GTSSLPVYDG	KFLTRVERVI	VVSMNYRVGA	LGFLAFPGNS	EAPGNMGLFD
CAT	TPKPKNATVM	IWIYGGGFQT	GTSSLPVYDG	KFLARVERVI	VVSMNYRVGA	LGFLALPGNP	EVPGNMGLFD
HORSE	APKPKNATVM	IWIYGGGFQT	GTSSLPVYDG	KFLARVERVI	VVSMNYRVGA	LGFLALSEN	EAPGNMGLFD

	180	190	200	210	220	230	240
HUMAN WT	QQLALQWVQK	NIAAFGGNFK	SVTLFGESAG	AASVSLHLLS	PGSHSLFTRA	ILQSGSFNAP	WAVTSLYEAR
HUMAN A	-----	-----	-----	-----	-----	-----	-----
HUMAN J	-----	-----	-----	-----	-----	-----	-----
HUMAN K	-----	-----	-----	-----	-----	-----	-----
RAT	QQLALQWVQK	NIAAFGGNPK	SVTLFGESAG	AASVSLHLLC	PQSYPLFTRA	ILESGSSNAP	WAVKHPEEAR
CAT	QQLALQWVQK	NIAAFGGNPK	SVTLFGESAG	AGSVSLHLLS	PRSQPLFTRA	ILQSGSSNAP	WAVMSLDEAK
HORSE	QQLALQWVQK	NIAAFGGNPR	SVTLFGESAG	AASVSLHLLS	PRSQPLFTRA	ILQSGSSNAP	WAVTSLYEAR

	250	260	270	280	290	300	310
HUMAN WT	NRTLNLAKLT	GCSRENETEI	IKCLRNKDPQ	EILLNEAFV	PYGTPLSVNF	GPTVDGDFLT	DMPDILLELG
HUMAN A	-----	-----	-----	-----	-----	-----	-----
HUMAN J	-----	-----	-----	-----	-----	-----	-----
HUMAN K	-----	-----	-----	-----	-----	-----	-----
RAT	NRTLTLAKFI	GCSKENEKEI	ITCLRSKDPQ	EILLNEKLVL	PSDSIRSINF	GPTVDGDFLT	DMPHTLLQLG
CAT	NRTLTLAKFI	GCSKENDTEI	IKCLRNKDPQ	EILLNELLVV	PSDTLLSVNF	GPVVDGDFLT	DMPDTLLQLG
HORSE	NRTLTLAKRM	GCSRDNETEM	IKCLRDKDPQ	EILLNEVFVV	PYDTLLSVNF	GPTVDGDFLT	DMPDTLLQLG

Figure 4A

9/11

	320	330	340	350	360	370	380
HUMAN WT	QFKKTQILVG	VNKDEGTAFL	VYGAPGFSKD	NNSIITRKEF	QEGLKIFFPG	VSEFGKESIL	FHYTDWVDDQ
HUMAN A	-----	-----	-----	-----	-----	-----	-----
HUMAN J	-----	-----	-----	-----	-----	-----	-----
HUMAN K	-----	-----	-----	-----	-----	-----	-----
RAT	KVKTAQILVG	VNKDEGTAFL	VYGAPGFSKD	NDSLITRREF	QEGLNMYFPG	VSSLGKEAIL	FYYVDWLGDQ
CAT	QFKKTQILVG	VNKDEGTAFL	VYGAPGFSKD	NDSIITRKEF	QEGLKIYFPG	VSEFGREAIL	FYYVDLLDDQ
HORSE	QFKRTQILVG	VNKDEGTAFL	VYGAPGFSKD	NNSIITRKEF	QEGLKIFFPR	VSEFGRESIL	FHYMDWLDDQ

	390	400	410	420	430	440	450
HUMAN WT	RPENYREALG	DVVGDFNFIC	PALEFTKKFS	EWGNNAFFYY	FEHRSSKLPW	PEWMGVMHGY	EIEFVFGGLPL
HUMAN A	-----	-----	-----	-----	-----	-----	-----
HUMAN J	-----	-----	-----	-----	-----	-----	-----
HUMAN K	-----	-----	-----	-----	-----	-----	-----
RAT	TPEVYREAFD	DIIGDYNIIIC	PALEFTKKFA	ELEINAFFYY	FEHRSSKLPW	PEWMGVMHGY	EIEFVFGGLPL
CAT	RAEKYREALD	DVLGDYNIIC	PALEFTTKFS	ELGNNAFFYY	FEHRSSQLPW	PEWMGVMHGY	EIEFVFGGLPL
HORSE	RAENYREALD	DVVGDFNIIC	PALEFTRKFS	ELGNDAFFYY	FEHRSTKLPW	PEWMGVMHGY	EIEFVFGGLPL

	460	470	480	490	500	510	520
HUMAN WT	ERRDNYTKAE	EILSRISIVKR	WANFAKYGNP	NETQNNSTSW	PVFKSTEQKY	LTLNTESTRI	MTKLRAQQCR
HUMAN A	-----	-----	-----	-----	-----	-----	-----
HUMAN J	-----	-----	-----	-----	-----	-----	-----
HUMAN K	-----	-----	-----	-----	-----	-----	-----
RAT	ERRVNYTRAE	EIFSRISIMKT	WANFAKYGHP	NGTQGNSTVW	PVFTSTEQKY	LTLNTEKSKI	NSKLRAQQCQ
CAT	ERRVNYTRAE	EILSRISIMNY	WANFAKYGNP	NGTQNNSTRW	PAFRSTDQKY	LTLNAESPKV	YTKLRAQQCR
HORSE	ERRVNYTRAE	EILSRISIMKR	WANFAKYGNP	NGTQNNSTRW	PVFKSTEQKY	LTLNTESPKV	YTKLRAQQCR

	530	540	550	560	570	574
HUMAN WT	FWTSFFPKVL	EMTGNIDEAE	WEWKAGFHRW	NNYMDWKNQ	FNDYTSKKES	CVGL
HUMAN A	-----	-----	-----	-----	-----	---
HUMAN J	-----	-----	-----	-----	-----	---
HUMAN K	-----	-----	-----	-----	-----	---
RAT	FWRLFFPKVL	EITGDIDERE	QEWKAGFHRW	SNYMDWKNQ	FNDYTSKKES	CTDL
CAT	FWTLFFPKVL	EMTGNIDEAE	REWRAGFYRW	NNYMDWKNQ	FNDYTSKKES	CAGL
HORSE	FWTLFFPKVL	ELTGNIDEAE	REWKAGFHRW	NNYMDWKNQ	FNDYTSKKES	CSDF

Figure 4B

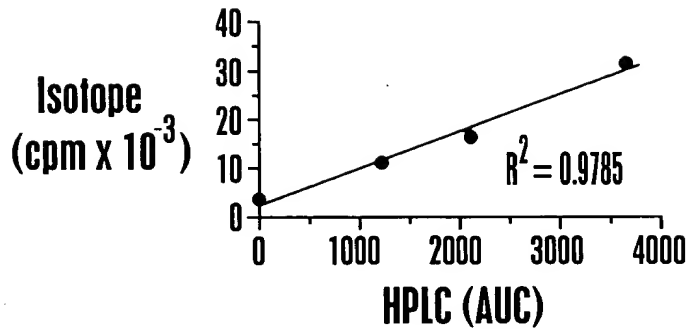


Figure 5A

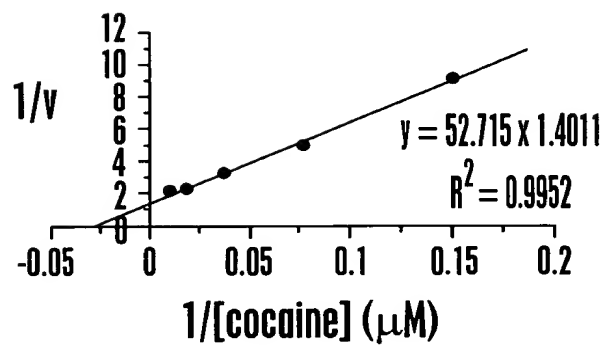


Figure 5B

1.01090" 6E4B4260